

Table 12: IRES Sequences

SEQ ID NO:___ A 519 base pair IRES obtainable from encephelomyocarditis virus (EMCV).

1 GACGTCGACTAAATCCGGTTATTTTCCACCATATTGCCGTCTTTTGGCAA
 SalI
 51 TGTGAGGGCCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCCTAGGG
 101 GTCTTTCCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAG
 151 GAAGCAGTTCCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGAC
 201 CCTTTGTCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCC
 251 AAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAAGTGC
 301 CACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAATGGCTCTCCTCAAG
 351 CGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGG
 401 GATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGG
 451 TTAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTTCCTTTGA
 SalI
 501 AAAACACGATGTCGACGTC

SEQ ID NO:___ An IRES obtainable from vascular endothelial growth factor (VEGF).

1 ACGTAGTTCGACAGCGCAGAGGCTTGGGGCAGCCGAGCGGCAGCCAGGCCC
 SalI
 51 CGGCCCGGGCCTCGGTTCCAGAAGGGAGAGGAGCCCGCAAGGCGCGCAA
 101 GAGAGCGGGCTGCCTCGCAGTCCGAGCCGGAGAGGGAGCGCGAGCCGCGC
 151 CGGCCCGGACGGCCTCCGAAACCATGGTTCGACACGTA
 SalI

SEQ ID NO:___ A 5'UTR region of HCV.

1
 30 GCCAGCCCCCTGATGGGGGCGACACTCCGCCATGAATCACTCCCCTGTGAGGAACTACTG
 61
 TCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGAC
 121 CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG
 181 GACGACCGGGTCCTTTCTTGGATTAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCC
 35 241 GCAAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGGCCTTGTGGTACTGCCTGATAGG
 301 GTGCTTGCAGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACC (341)

SEQ ID NO: __ A 5'UTR region of BiP SEQ ID NO:4

1
CCCCGGGGTCACTCCTGCTGGACCTACTCCGACCCCCTAGGCCGGGAGTGAAGGCGGGACT
61
5 TGTGCGGTTACCAGCGGAAATGCCTCGGGGTCAGAAGTCGCAGGAGAGATAGACAGCTGC
121 TGAACCAATGGGACCAGCGGATGGGGCGGATGTTATCTACCATTGGTGAACGTTAGAAAC
181 GAATAGCAGCCAATGAATCAGCTGGGGGGGCGGAGCAGTGACGTTTATTGCGGAGGGGGC
241 CGCTTCGAATCGGCGGCGGCCAGCTTGGTGGCCTGGGCCAATGAACGGCCTCCAACGAGC
301 AGGGCCTTCACCAATCGGCGGCCTCCACGACGGGGCTGGGGGAGGGTATATAAGCCGAGT
10 361 AGGCGACGGTGAGGTGCAGCGCCGCCAAGACAGCACAGACAGATTGACCTATTGGGGTGT
421 TTCGCGAGTGTGAGAGGGAAGCGCCGCGGCCTGTATTTCTAGACCTGCCCTTCGCTTGGT
481 TCGTGGCGCCTTGTGACCCCCGGGCCCCCTGCCGCCTGCAAGTCGAAATTGCGCTGTGCTCC
541 TGTGCTACGGCCTGTGGCTGGACTGCCTGCTGCTGCCCAACTGGCTGGCAAGATG (595)

SEQ ID NO: __ A 5'UTR of PDGF SEQ ID NO:5

1
GTTTGACCTCTCCCTGCCCCGGGTGCTCGAGCTGCCGTTGCAAAGCCAACCTTTGGAAAAA
61
20 GTTTTTTGGGGGAGACTTGGGCCTTGAGGTGCCAGCTCCGCGCTTCCGATTTTGGGGG
121 CTTTCCAGAAAAATGTTGCAAAAAAGCTAAGCCGGCGGGCAGAGGAAAACGCCTGTAGCCG
181 GCGAGTGAAGACGAACCATCGACTGCCGTGTTCTTTTCTCTTGGAGGTTGGAGTCCCC
241 TGGGCGCCCCCACACCCCTAGACGCCTCGGCTGGTTCGCGACGCAGCCCCCGGCCGTGG
301 ATGCTGCACTCGGGCTCGGGATCCGCCAGGTAGCCGGCCTCGGACCCAGGTCTGCGCC
361 CAGGTCCTCCCCTGCCCCCAGCGACGGAGCCGGGGCCGGGGGCGGCGGCGCGGGGGCA
25 421 TGCGGGTGAGCCGCGGCTGCAGAGGCCTGAGCGCCTGATCGCCGCGGACCTGAGCCGAGC
481 CCACCCCCCTCCCCAGCCCCCACCCTGGCCGCGGGGGCGGCGCGCTCGATCTACGCGTC
541 CGGGGCCCCGCGGGGCCGGGCCCCGGAGTCGGCATG (575)

Table 13: Literature References For IRES

IRES Host	Example	Reference
Picornavirus	HAV	Glass et al., 1993. Virol-193:842-852
	EMCV	Jang & Wimmer, 1990. Gene Dev 4:1560-1572
	Poliovirus	Borman et al., 1994. EMBO J 13:3149-3157
HCV and pestivirus	HCV	Tsukiyama-Kohara et al., 1992. J Virol 66:1476-1483
	BVDV	Frolov I et al., 1998. RNA. 4:1418-1435
Leishmania virus	LRV-1	Maga et al., 1995. Mol Cell Biol 15:4884-4889
Retroviruses	MoMLV VL30 (Harvey murine sarcoma virus)	Torrent et al., 1996. Hum Gene Ther 7:603-612
	REV	Lopez-Lastra et al., 1997. Hum Gene Ther 8:1855-1865
Eukaryotic mRNA	BiP	Macejak & Sarnow, 1991. Nature 353:90-94
	antennapedia mRNA	Oh et al., 1992. Gene & Dev 6:1643-1653
	FGF-2	Vagner et al., 1995. Mol Cell Biol 15:35-44
	PDGF-B	Bernstein et al., 1997. J Biol Chem 272:9356-9362
	IGFII	Teerink et al., 1995. Biochim Biophys Acta 1264:403-408
	eIF4G	Gan & Rhoads, 1996. J Biol Chem 271:623-626
	VEGF	Stein et al., 1998. Mol Cell Biol 18:3112-3119; Huez et al., 1998. Mol Cell Biol 18:6178-6190

Table 14: TRE Sequences

Nucleotide sequence of a human uroplakin II 5' flanking region. Position +1 (the translational start site) is denoted with an asterisk. SEQ ID NO: __ (number 1 of

SEQ ID NO: __ corresponds to position -2239 with respect to the translational start site).

5	TCGATAGGTA 1	CCCACTATAG	GGCACGCGTG	GTCGACGGCC	CGGGCTGGTC 50
	TGGCAACTTC 51	AAGTGTGGGC	CTTTCAGACC	GGCATCATCA	GTGTTACGGG 100
10	GAAGTCACTA 101	GGAATGCAGA	ATTGATTGAG	CACGGTGGCT	CACACCTGTA 150
	ATCCCAACAC 151	TCTGGGAGGC	CAAGGCAGGT	GGATCACTTG	TGGTCAGGAG 200
15	TTTGAGACCA 201	GCCTGGCCAA	CATGGTGAAA	CCTCATCTCT	ACTAAAAATA 250
	CAAAAATTAG 251	CTGGGAATGG	TGGCACATGC	CTATAATCCC	AGTTACTCAG 300
20	GAGGCTGAGG 301	CAGGAGAATC	ATTTGAACCT	GGGAGGCAGA	GGTTGCAGTG 350
	AGCCGAGATC 351	ACGCCACTGC	ACTCCAGCCT	GGGTGACACA	GCGAGACTCT 400
25	GTCTCAAAAA 401	AAAAAAAATG	CAGAATTTCA	GGCTTCACCC	CAGACCCACT 450
	GCATGACTGC 451	ATGAGAAGCT	GCATCTTAAC	AAGATCCCTG	GTAATTCATA 500
30	CGCATATTAA 501	ATTTGGAGAT	GCACTGGCGT	AAGACCCTCC	TACTCTCTGC 550
	TTAGGCCCAT 551	GAGTTCTTCC	TTTACTGTCA	TTCTCCACTC	ACCCCAAACCT 600
40	TTGAGCCTAC 601	CCTTCCCACC	TTGGCGGTAA	GGACACAACC	TCCCTCACAT 650
	TCCTACCAGG 651	ACCCTAAGCT	TCCCTGGGAC	TGAGGAAGAT	AGAATAGTTC 700
45	GTGGAGCAAA 701	CAGATATACA	GCAACAGTCT	CTGTACAGCT	CTCAGGCTTC 750
	TGGAAGTTCT 751	ACAGCCTCTC	CCGACAAAGT	ATTCCACTTT	CCACAAGTAA 800
50	CTCTATGTGT 801	CTGAGTCTCA	GTTTCCACTT	TTCTCTCTCT	CTCTCTCTCT 850

5
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CAACTTTCTG 851	AGACAGAGTT	TCACTTAGTC	GCCCAGGCTG	GAGTGCAGGG 900
GCACAATCTC 901	GGCTCACTGC	AACCTCCACC	TCCTGGGTTC	AAGTGTCTTCT 950
CCTGTCTCAG 951	CCTCCCGAGT	AGCTGGGATT	ACAGGCACAC	ACCACCGCGT 1000
TAGTTTTTGT 1001	ATTTTTGGTA	GAGATGGTGT	TTCGCCATAT	TGGCCAGGCT 1050
GATCTCGAAC 1051	TCCTGACCTC	AGGTGATCCG	CCCACCTCGG	CCTCCCAAAG 1100
TGCTGGGATT 1101	ACAGGCATGA	GCCACCACGC	CCGGCTGATC	TCTTTTCTAT 1150
TTTAATAGAG 1151	ATCAAACCTCT	CTGTGTTGCC	TAGGCTGGTC	TTGAACTCCT 1200
GGCCTCGAGT 1201	GATCCTCCCA	CCTTGGCCTC	CCAAAGTGTT	GAGATTACAG 1250
GCATGAGCCA 1251	CTGTGCCTGG	CCTCAGTTCT	ACTACAAAAG	GAAGCCAGTA 1300
CCAGCTACCA 1301	CCCAGGGTGG	CTGTAGGGCT	ACAATGGAGC	ACACAGAACC 1350
CCTACCCAGG 1351	GCCCCGAAGA	AGCCCCGACT	CCTCTCCCCT	CCCTCTGCCC 1400
AGAACTCCTC 1401	CGCTTCTTTC	TGATGTAGCC	CAGGGCCGGA	GGAGGCAGTC 1450
AGGGAAGTTC 1451	TGTCTCTTTT	TCATGTTATC	TTACGAGGTC	TCTTTTCTCC 1500
ATTCTCAGTC 1501	CAACAAATGG	TTGCTGCCCA	AGGCTGACTG	TGCCCACCCC 1550
CAACCCCTGC 1551	TGGCCAGGGT	CAATGTCTGT	CTCTCTGGTC	TCTCCAGAAG 1600
TCTTCCATGG 1601	CCACCTTCGT	CCCCACCCTC	CAGAGGAATC	TGAAACCGCA 1650
TGTGCTCCCT 1651	GGCCCCCACA	GCCCCGCTCT	CTCCCAGAGC	AGCAGTACCT 1700
AAGCCTCAGT 1701	GCACTCCAAG	AATTGAAACC	CTCAGTCTGC	TGCCCCCTCC 1750

	CACCAGAATG	TTTCTCTCCC	ATTCTTACCC	ACTCAAGGCC	CTTTCAGTAG	1800
	1751					
5	CCCCTTGGAG	TATTCTCTTC	CTACATATCA	GGGCAACTTC	CAAACCTCATC	1850
	1801					
	ACCCTTCTGA	GGGGTGGGGG	AAAGACCCCC	ACCACATCGG	GGGAGCAGTC	1900
	1851					
10	CTCCAAGGAC	TGGCCAGTCT	CCAGATGCCC	GTGCACACAG	GAACACTGCC	1950
	1901					
	TTATGCACGG	GAGTCCCAGA	AGAAGGGGTG	ATTTCTTTCC	CCACCTTAGT	2000
	1951					
	TACACCATCA	AGACCCAGCC	AGGGCATCCC	CCCTCCTGGC	CTGAGGGCCA	2050
	2001					
20	GCTCCCCATC	CTGAAAACC	TGTCTGCTCT	CCCCACCCCT	TTGAGGCTAT	2100
	2051					
	AGGGCCCAAG	GGGCAGGTTG	GA CTGGATT C	CCCTCCAGCC	CCTCCCGCCC	2150
	2101					
25	CCAGGACAAA	ATCAGCCACC	CCAGGGGCAG	GGCCTCACTT	GCCTCAGGAA	2200
	2151					
	CCCCAGCCTG	CCAGCACCTA	TTCCACCTCC	CAGCCCAGCA		2239
	2201					
30						

Nucleotide sequence of a mouse uroplakin II 5' flanking region. The translational start site is denoted with an asterisk. SEQ ID NO:___ (number 1 of SEQ ID NO:6___corresponds to position -3592 with respect to the translational start site).

	CTCGAGGATCTCGGCCCTCTTTCTGCATCCTTGTCCTAAATCATTTTCAT	50
	1	
40	ATCTTGCTAGACCTCAGTTTGAGAGAAACGAACCTTCTCATTTTCAAGTT	100
	51	
	GAAAAAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACAC	150
	101	
45	TCACCACTACGAGTACAATGGCCACCATTAGTGCTGGCATGCCCCAGGAG	200
	151	
50	ACAGGCATGCATATTATTCTAGATGACTGGGAGGCAGAGGGGTGGCCTAG	250
	201	

TGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAATT
251 300

5 CCTCAGGCCGCGAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGCA
301 350

GTCCGGAACAGGAGGTCCATTTGAGAGCTGACTGAGCAGAAGAGGAAAGT
351 400

10 GAAGAACTTCTGGGGCAAGAGCTTACCCTACTTTACAGCTTTGTTGTCTT
401 450

15 CTTTACTCCAGGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCTTGAG
451 500

GAACATATGTGTAAGGAGGAAGGAGAGGGAAGTTGAGGGAGTTAAGACTC
501 550

20 AAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAGAGAG
551 600

ACTCCAGACATTGGCCCTGGTTCCTTCTTGCCACTGTGAAACCCTCCA
601 650

25 GAGGAACTGAGTGCTGTGGCTTTAAATGATCTCAGCACTGTCAGTGAAGC
651 700

GCTCTGCTCAAAGAGTTATCCTCTTGCTCCTGTGCCGGGGCCTCCCCCTC
701 750

30 CTCTCAGCTCCCCAAACCCTTCTCAGCCACTGTGATGGCATAATTAGATGC
751 800

35 GAGAGCTCAGACCGTCAGGTCTGCTCCAGGAACCACCCATTTTCCCCAAC
801 850

CCCAGAGAAAGGTCCTAGTGGAAGAGTGGGGGCCACTGAAGGGCTGATGG
851 900

40 GGTTCCTGTCCTTTCCCCCATGCTGGGTGGACTTAAAGTCTGCGATGTGTG
900 950

TAGGGGGTAGAAGACAACAGAACCTGGGGGCTCCGGCTGGGAGCAGGAGG
951 1000

45 AACTCTCACCAGACGATCTCCAAATTTACTGTGCAATGGACGATCAGGAA
1001 1050

50 ACTGGTTCAGATGTAGCTTCTGATACAGTGGGTCTGAGGTAAAACCCGAA
1051 1100

ACTTAATTTCTTTCAAAAATTTAAAGTTGCATTTATTATTTTATATGTGT
1101 1150

5 GCCCATATGTGTGCCACAGTGTCTATGTGGAGGTCAGAGGGCAAGTTGTG
1151 1200

GGCATTGGCTCTCTCCTTTTCATAATGTGGCTTCTGGGGACCAAAATGTCA
1201 1250

10 GGCATGGTGGCAAGAGCTTTTACCTGTTGAGCCATCTCATGGTTTCGTAA
1251 1300

15 AACTTCCTATGACGCTTACAGGTAACGCAGAGACACAGACTCACATTTGG
1301 1350

AGTTAGCAGATGCTGTATTGGTGTAAACACTCATAACAGACACACACAC
1351 1400

20 ATACTCATAACACACACACACACTTATCACATGCACACACATACTCGTA
1401 1450

TACACACAGACACACACACATGCACTCTCACATTTCACATATTCATACACA
1451 1500

25 TCCACACACACACTCATCCACACACACAGACACACATACTCATCCACACA
1501 1550

30 CACACACACACATACTCATAACACACACAGACACACATACTCATACACA
1551 1600

CACACAGACACACACATATAATCATAACACAGACACACTCATACATG
1601 1650

35 TGCACACACACACTCATCCACACACACACTCATACACACACACTCA
1651 1700

TACACACACACACTCATACACACACACAGAGGTTTTTCTCAGGCTGCCT
1701 1750

40 TTGGGTGGAGACTGGAAGTGAATTTCTGTTTTTCAGCTCCTTGGCTTTTTG
1751 1800

45 TCCCTTTAGATGAGATCTCCTCCTCACTTTACACACAGAAAGATCACACA
1801 1850

CGAGGGAGAACTGGCGGTGCGGAAGAGGGCTACACGGTAGGGTGTGAGGG
1851 1900

50 TCAGGAGATCTTCCTGGCAAGTCTCAAACCTCCACATAGCACAGTGTTTA

	1901	1950
	CGTGAGGATTTAGGAGGAATCAGGAAGAGGATTGGTTTACTGCAGAGCAG	
	1951	2000
5	ACCATATAGGTCCACTCCTAAGCCCCATTTGAAATTAGAAGTGAGACAGT	
	2001	2050
	GTGGGATAAAAAGAGCAGATCTCTGGTCACATTTTTAAAGGGATATGAGG	
10	2051	3000
	GTCCTGTGCCTTTAAGCCTTCCCATCTCCCTCCAATCCCCCCTCACCTTC	
	2101	2150
15	CCCACCCTAACCTCCCCAGGTTTCTGGAGGAGCAGAGTTGCGTCTTCTC	
	2151	2200
	CCTGCCCTGCCGAGCTGCTCACTGGCTGCTCTAGAGGCTGTGCTTTGCGG	
	2201	2250
20	TCTCCATGGAAACCATTAGTTGCTAAGCAACTGGAGCATCATCTGTGCTG	
	2251	2300
	AGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCACGCCCCCTGCAG	
25	2301	2350
	CCACTTTGCAGTGACAAGCCTGAGTCTCAGGTTCTGCATCTATAAAAACG	
	2351	2400
30	AGTAGCCTTTTCAGGAGGGCATGCAGAGCCCCCTGGCCAGCGTCTAGAGGA	
	2401	2450
	GAGGTGACTGAGTGGGGCCATGTCACTCGTCCATGGCTGGAGAACCTCCA	
	2451	2500
35	TCAGTCTCCCAGTTAGCCTGGGGCAGGAGAGAACCAGAGGAGCTGTGGCT	
	2501	2550
	GCTGATTGGATGATTTACGTACCCAATCTGTTGTCCCAGGCATCGAACCC	
40	2551	2600
	CAGAGCGACCTGCACACATGCCACCGCTGCCCCGCCCTCCACCTCCTCTG	
	2601	2650
45	CTCCTGGTTACAGGATTGTTTTGTCTTGAAGGGTTTTGTTGTTGCTACTT	
	2651	2700
	TTTGCTTTGTTTTTTCTTTTTTAACATAAGGTTTCTCTGTGTAGCCCTAG	
50	2701	2750

CTGTCCTGGAAC TCACTCTGTAGACCAGGCTGGCCTCAAAC TCAAGAAATC
2751 2800

5 CACCTTCCTCCCAAGTGCTGGGATTAAAGGCATTTCGCACCATCGCCCAGC
2801 2850

CCCCGGTCTTGTTTCCTAAGGTTTTCTTGCTTTACTCGCTACCCGTTGCA
2851 2900

10 CAACCGCTTGCTGTCCAAGTCTGTTTGTATCTACTCCACCGCCCACTAGC
2901 2950

CTTGCTGGACTGGACCTACGTTTACCTGGAAGCCTTCACTAACTTCCCTT
2951 3000

15 GTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCCTCCGCTT
3001 3050

20 CTCCCAGAGTCGCAGTTTCTTAGGCCTCAGTTAAATACCAGAATTGGATC
3051 3100

TCAGGCTCTGCTATCCCCACCCTACCTAACCAACCCCTCCTCTCCCATC
3101 3150

25 CTTACTAGCCAAAGCCCTTTCAACCCTTGGGGCTTTTCCTACACCTACAC
3151 3200

30 ACCAGGGCAATTTTAGAACTCATGGCTCTCCTAGAAAACGCCTACCTCCT
3201 3250

TGGAGACTGACCCTCTACAGTCCAGGAGGCAGACACTCAGACAGAGGAAC
3251 3300

35 TCTGTCCTTCAGTCGCGGGAGTTCCAGAAAGAGCCATACTCCCCTGCAGA
3301 3350

GCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGCCGAGGG
3351 3400

40 CCAGCTCCCCAGAATGAAAAACCTGTCTGGGGCCCCCTCCCTGAGGCTACA
3401 3450

GTCGCCAAGGGGCAAGTTGGACTGGATTCCCAGCAGCCCCTCCCACTCCG
3451 3500

45 AGACAAAATCAGCTACCCTGGGGCAGGCCTCATTGGCCCCAGGAAACCCC
3501 3550
AGCCTGTCAGCACCTGTTCCAGGATCCAGTCCCAGCGCAGTA
3551

50 3592

AFP-TRE. SEQ ID NO:___.

1 GCATTGCTGTGAACTCTGTACTTAGGACTAACTTTGAGCAATAACACACATAGATTGAG
5 61 GATTGTTTGCTGTTAGCATACAACTCTGGTTCAAAGCTCCTCTTTATTGCTTGTCTTGG
121 AAAATTTGCTGTTCTTCATGGTTTCTCTTTTCACTGCTATCTATTTTCTCAACCACTCA
10 181 CATGGCTACAATAACTGTCTGCAAGCTTATGATTCCCAAATATCTATCTCTAGCCTCAAT
241 CTTGTTCCAGAAGATAAAAAGTAGTATTCAAATGCACATCAACGTCTCCACTTGGAGGGC
15 301 TTAAAGACGTTTCAACATACAAACCGGGAGTTTTGCCTGGAATGTTTCCTAAAAATGTGT
361 CCTGTAGCACATAGGGTCCTCTTGTTCCTTAAATCTAATTACTTTTAGCCCAGTGCTCA
421 TCCCACCTATGGGGAGATGAGAGTGAAAAGGGAGCCTGATTAATAATTACACTAAGTCAA
20 481 TAGGCATAGAGCCAGGACTGTTTGGGTAACTGGTCACTTTATCTTAACTAAATATATC
541 CAAAACCTGAACATGTACTTAGTTACTAAGTCTTTGACTTTATCTCATTCATACCACTCAG
25 601 CTTTATCCAGGCCACTTATGAGCTCTGTGTCTTGAACATAAAATACAAATAACCGCTAT
661 GCTGTTAATTATTGGCAAATGTCCCATTTTCAACCTAAGGAAATACCATAAAGTAACAGA
721 TATACCAACAAAAGGTTACTAGTTAACAGGCATTGCCTGAAAAGAGTATAAAAGAATTTTC
30 781 AGCATGATTTTCCATATTGTGCTTCCACCACTGCCAATAACA (822)

Probasin -TRE SEQ ID NO:___

-426
5' -AAGCTTCCACAAGTGCATTTAGCCTCTCCAGTATTGCTGATGAATCCACAGT
40 TCAGGTTCAATGGCGTTCAAACTTGATCAAAAATGACCAGACTTTATATTTA
CACCAACATCTATCTGATTGGAGGAATGGATAATAGTCATCATGTTTAAACAT
45 CTACCATTCCAGTTAAGAAAATATGATAGCATCTTGTTCCTTAGTCTTTTCTTA
ARE-1
ATAGGGACATAAAGCCCACAAATAAAAAATATGCCTGAAGAATGGGACAGGC
50 ATTGGGCATTGTCCATGCCTAGTAAAGTACTCCAAGAACCTATTTGTATACTA
ARE-2
GATGACACAATGTCAATGTCTGTGTACAACGCCAACTGGGATGCAAGACAC
55 TGCCCATGCCAATCATCCTGAAAAGCAGCTATATAAAAGCAGGAAGCTACTCT
CAAT box TATAA box

+1

+28

GCACCTTGTTCAGTAGGTCCAGATACCTACAG-3'
Transcription site

5

Tyrosinase-TRE SEQ ID NO: __

PinAl end -1956

10

1 CCGGTGAAAATGATAAGTTGAATTCTGTCTTCGAGAACATAGAAAAGAA
51 TTATGAAATGCCAACATGTGGTTACAAGTAATGCAGACCCAAGGCTCCCC
101 AGGGACAAGAAGTCTTGTGTTAACTCTTGTGGCTCTGAAAGAAAGAGAG
151 AGAGAAAAGATTAAGCCTCCTTGTGGAGATCATGTGATGACTTCCTGATT
201 CCAGCCAGAGCGAGCATTTCATGGAACTTCTCTTCTCTTCTCGAG -1716
-231 251 ATTACTAACCTTATTGTTAATATTCTAACCATAGAATTAAGTATTAACT
301 GGTGAATAGAGTTTTTCACTTTAACATAGGCCTATCCCACTGGTGGGATA
15 351 CGAGCCAATTTCGAAAGAAAAGTCAAGTCATGTGCTTTTCAGAGGATGAAA
401 GCTTAAGATAAAGACTAAAAGTGTGTTGATGCTGGAGGTGGGAGTGGTATT
451 ATATAGGTCTCAGCCAAGACATGTGATAATCACTGTAGTAGTAGCTGGAA
501 AGAGAAATCTGTGACTCCAATTAGCCAGTTCCTGCAGACCTTGTGA + 65

PinAl end

20

Human glandular kallikrein-TRE SEQ ID NO: __

25

gaattcagaa ataggggaag gttgaggaag gacactgaac tcaaagggga tacagtgatt 60
ggtttatttg tcttctcttc acaacattgg tgctggagga attcccaccc tgagggtatg
120
aagatgtctg aacacccaac acatagcact ggagatatga gctcgacaag agtttctcag
180
ccacagagat tcacagccta gggcaggagg aactgtacg ccaggcagaa tgacatggga
240
attgcgctca cgattggcctt gaagaagcaa ggactgtggg aggtgggctt tgtagtaaca
300
35 agagggcagg gtgaactctg attcccatgg gggaatgtga tggctctggt acaaattttt
360
caagctggca gggaataaaa cccattacgg tgaggacctg tggagggcgg ctgcccacac
40 420
tgataaagga aatagccagg tgggggcctt tcccattgta ggggggacat atctggcaat
480
45 agaagccttt gagacccttt aggggtacaag tactgaggca gcaaataaaa tgaaatctta
540
tttttcaact ttatactgca tgggtgtgaa gatataatttg tttctgtaca gggggtgagg
600

50

gaaaggaggg gaggaggaaa gttcctgcag gtctggtttg gtcttgtgat ccagggggtc
660

5 ttggaactat ttaaattaaa ttaaattaaa acaagcgact gttttaaaatt aaattaaatt
720

aaattaaatt ttactttatt ttatcttaag ttctgggcta catgtgcagg acgtgcagct
780

10 ttgttacata ggtaaacgtg tgccatgggtg gtttgctgta cctatcaacc catcacctag
840

gtattaagcc cagcatgcat tagctgtttt tcttgacgct ctccctctcc ctgactccca
900

15 caacaggccc cagtgtgtgt tgttccccctc cctgtgtcca tgtgttctca ttgttcagct
960

20 cccacttata agtgagaaca tgtgggtgtt ggttttctgt ttctgtgtta gtttgctgag
1020

gataatggct tccacctcca tccatgttcc tgcaaaggac gtgatcttat tcttttttat
1080

25 ggttgcatag aaattgtttt tacaaatcca attgatattg tatttaatta caagttaatc
1140

taattagcat actagaagag attacagaag atattaggta cattgaatga ggaaatatat
1200

30 aaaataggac gaaggtgaaa tattaggtag gaaaagtata atagttgaaa gaagtaaaaa
1260

35 aaaatatgca tgagtagcag aatgtaaaag aggtgaagaa cgtaatagtg acttttttaga
1320

ccagattgaa ggacagagac agaaaaattt taaggaattg ctaaaccatg tgagtgttag
1380

40 aagtacagtc aataacatta aagcctcagg aggagaaaag aataggaaaag gaggaaatat
1440

gtgaataaat agtagagaca tgtttgatgg attttaaaat atttgaaaga cctcacatca
1500

45 aaggattcat accgtgccat tgaagaggaa gatggaaaag ccaagaagcc agatgaaagt
1560

50 tagaaatatt attggcaaag cttaaagtgt aaaagtccta gagagaaaag atggcagaaa
1620

tattggcggg aaagaatgca gaacctagaa tataaattca tccaacagt ttggtagtgt
1680

55 gcagctgtag cctttttctag ataatacact attgtcatac atcgcttaag cgagtgtaaa
1740

atgggtctcct cactttatatt atttatatat ttatttagtt ttgagatgga gcctcgctct
1800

60

gtctcctagg ctggagtgca atagtgcgat accactcact gcaacctctg cctcctctgt
1860

5 tcaagtgatt ttcttacctc agcctcccgga gtagctggga ttacaggtgc gtgccaccac
1920

acccggctaa tttttgtatt tttttagag acggggtttt gccatgttgg ccaggtggt
1980

10 cttgaactcc tgacatcagg tgatccacct gccttggcct cctaaagtgc tgggattaca
2040

ggcatgagcc accgtgccc accactttat ttatttttta tttttatttt taaatttcag
2100

15 cttctatttg aaatacaggg ggcacatata taggattggt acatgggtat attgaactca
2160

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